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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/996,015	11/28/2001	Kerry E. Quinn	15966-581CIP (Cura-81 CIP	2939

7590 01/27/2005

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EXAMINER	
RAMIREZ, DELIA M	
ART UNIT	**PAPER NUMBER**
1652	

DATE MAILED: 01/27/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/996,015	QUINN ET AL.	
	Examiner	Art Unit	
	Delia M. Ramirez	1652	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *04 November 0404*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1 and 5-43* is/are pending in the application.

4a) Of the above claim(s) *5-28,30,31 and 33-43* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1,29,32* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *5/22/02,7/18/02*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *alignments*.

DETAILED ACTION

Status of the Application

Claims 1, 5-43 are pending.

Applicant's election without traverse of Group II, claims 1-4, 29, 32 drawn in part to the polypeptide of SEQ ID NO: 6, amendment of claim 1, and cancellation of claims 2-4, in a communication filed on 11/4/2004 are acknowledged.

Claims 5-28, 30, 31 and 33-43 are withdrawn from further consideration by the Examiner, 37 CFR 1.142(b), as being drawn to a non-elected invention.

Inventorship

1. In view of the papers filed 11/4/2004, the inventorship in this nonprovisional application has been changed by the deletion of inventors Mario W. Leite, Li Li and Steven K. Spaderma.

The application will be forwarded to the Office of Initial Patent Examination (OIPE) for issuance of a corrected filing receipt, and correction of the file jacket and PTO PALM data to reflect the inventorship as corrected.

Specification

2. The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. See particularly page 2, line 31 of the specification. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01.

Priority

3. Acknowledgment is made of a claim for domestic priority under 35 U.S.C. 119(e) to provisional application No. 60/175,534 filed on 01/11/2000, 60/159,613 filed on 10/14/1999, and 60/224,086 filed on 08/09/2000.

4. Acknowledgment is made of a claim for domestic priority under 35 U.S.C. 120 or 121 to US application No. 09/641,741 filed on 08/18/2000.

5. SEQ ID NO: 6 appears to have been first disclosed in U.S. Provisional Application No. 60/224,086 filed on 8/9/2000.

Information Disclosure Statement

6. The information disclosure statements (IDS) submitted on 5/22/2002 and 7/18/2002 are acknowledged. The submissions are in compliance with the provisions of 37 CFR 1.97. Accordingly, the information disclosure statements are being considered by the examiner.

Claim Objections

7. Claim 1 is objected to due to the recitation of "(c) the amino acid sequences given by SEQ ID NO: 6". For clarity and consistency, the term should be replaced with "(b) the amino acid sequence given by SEQ ID NO: 6". Appropriate correction is required.

Claim Rejections - 35 USC § 112, Second Paragraph

8. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

9. Claims 1, 29 and 32 rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

10. Claim 1 (claims 29 and 32 dependent thereon) is indefinite in the recitation of "mature form of the amino acid sequence given by SEQ ID NO: 6" for the following reasons. First, it is unclear as to what is a mature form of a sequence. As known in the art, sequences are graphical representations of the order in which nucleotides/amino acids are arranged in a molecule. Therefore, it is unclear as to what constitutes the mature form of a graphical representation. In addition, even if the term "mature form" refers to a polypeptide, and not a sequence, it is noted that while one of skill in the art would interpret the term "mature form" as referring to a polypeptide lacking a signal peptide or the N-terminal methionine, the specification describes the term "mature form" (page 22, lines 13-25), as one which encompasses not only a polypeptide lacking its signal peptide or the N-terminal methionine but a polypeptide subjected to any proteolytic cleavage event. As such, it is unclear if the intended meaning of the term is that generally used in the art or if the term encompasses any fragment of the polypeptide recited in the claim. It is suggested that the claim be amended to recite the specific amino acid residues which correspond to the desired fragment of the polypeptide of SEQ ID NO: 6 ("amino acids X-Y of the amino acid sequence given by SEQ ID NO: 6", or similar). For examination purposes, the claim will be interpreted as being directed in part to a polypeptide comprising any fragment of the polypeptide of SEQ ID NO: 6. Correction is required.

Claim Rejections - 35 USC § 101

11. 35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

12. Claims 1, 29 and 32 rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a substantial and specific asserted utility or a well established utility.

Claims 1, 29 and 32 are drawn to (1) the polypeptide of SEQ ID NO: 6, (2) polypeptides comprising any fragment of (1), and (3) compositions comprising (1) or (2).

Applicants refer to the polypeptide of SEQ ID NO: 6 as an aortic carboxypeptidase-like protein 2 (ACPL2; page 3, Summary of the Invention) and indicate that the polypeptides of the invention have sequence similarity to previously described members of the carboxypeptidase family. Applicants also indicate that the polypeptide of SEQ ID NO: 6 is highly homologous to a 734 amino acid long human protein, which in turn is moderately similar to a mouse metallocarboxypeptidase CPX-1. While Applicants have asserted a biological function for the polypeptide of SEQ ID NO: 6 as that of an aortic carboxypeptidase-like protein, the claimed invention does not meet the utility requirements for the following reasons. As noted in the specification (pages 1-2 of the specification), carboxypeptidases are involved in multiple biological processes and are very diverse. However, the specification fails to provide any clue as to (1) the specific biological function of the polypeptide of SEQ ID NO: 6, (2) the biological processes associated with the polypeptide of SEQ ID NO: 6, (3) disorders/diseases which are associated with the expression, or lack thereof, of the polynucleotide of SEQ ID NO: 5 (encodes the polypeptide of SEQ ID NO: 6), or (4) which are the substrates/targets of the alleged aortic carboxypeptidase-like protein. Furthermore, it is noted that as indicated in the specification (page 11, last paragraph, page 12, line 1), the ACPL proteins of the invention may lack enzymatic cleavage function (i.e. carboxypeptidase activity) since they appear to lack several active site residues which are important for catalytic activity. Layne et al. (J.Biol. Chem. 273(25):15654-15660, 1998; cited in the specification; page 11, Table I) discloses a human aortic carboxypeptidase-like protein which has a carboxypeptidase-like domain of approximately 500 amino acids at its C-terminus but lacks carboxypeptidase activity (page 15659, left column, second paragraph), and suggest that while it may be catalytically inactive, it can bind

to other proteins via the carboxypeptidase-like domain. Layne et al. also disclose that the human aortic carboxypeptidase-like protein plays a role in differentiated vascular smooth cells (Abstract, last sentence). Since (1) according to the specification and the teachings of Layne et al., an aortic carboxypeptidase-like protein may not be active as a carboxypeptidase, (2) the specification is completely silent as to any additional non-enzymatic function associated to the polypeptide of SEQ ID NO:6, such as those indicated by Layne et al. in regard to their protein, and (3) there is no clue as to the specific function of the closest structural homolog (SPTREMBL Q9NUB5, also labeled Q96SM3) other than being described as being a CPX-1 homolog with no carboxypeptidase activity (see attached alignment of Q96SM3 against the polypeptide of SEQ ID NO:6; immediately after the last literature citation under "Function"), one of skill in the art cannot determine the actual biological function of the claimed polypeptide.

Applicant's asserted utility for the polypeptide of SEQ ID NO: 6 (aortic carboxypeptidase-like protein), particularly in view of a lack of knowledge as to its specific biological function, the biological processes associated with the polypeptide of SEQ ID NO: 6, disorders/diseases which are associated with the abnormal expression of the polynucleotide of SEQ ID NO: 5, or the substrates/targets associated with the polypeptide of SEQ ID NO: 6, is not specific or substantial since it will require or constitute carrying out further research to identify or reasonably confirm a "real world" context of use. See e.g., *Brenner v. Manson,* 383 U.S. 519, 148 USPQ 689 (Sup. Ct. 1966). The instant situation is analogous to the lack of substantial utility examples provided by MPEP § 2107.01 in that basic research is required to study the properties of the claimed polypeptides as well as the mechanisms in which the claimed polypeptides are involved. Since the instant specification does not disclose an specific and substantial "real world" use for the polypeptide of SEQ ID NO: 6, then the claimed invention as disclosed does not meet the requirements of 35 U.S.C. §101 as being useful.

13. Claims 1, 29 and 32 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

Claim Rejections - 35 USC § 112, First Paragraph

14. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

15. Claims 1, 29 and 32 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claims 1, 29 and 32 are directed in part to a polypeptide of any function comprising any fragment of the polypeptide of SEQ ID NO: 6, and compositions thereof. See Claim Rejections under 35 USC 112, second paragraph for claim interpretation. While the specification discloses the structure of the polypeptide of SEQ ID NO: 6 and indicates that said polypeptide is an aortic carboxypeptidase-like protein (ACPL) 2, the specification fails to disclose the structure and function of other polypeptides comprising any fragment of the polypeptide of SEQ ID NO: 6. The genus of polypeptides claimed is a large variable genus with the potentiality of encompassing many different functions. As taught by the art, even highly structurally homologous species may not share the same function. Witkowski et al. (Biochemistry 38:11643-11650, 1999) teaches that one amino acid substitution transforms a β–ketoacyl synthase into a malonyl decarboxylase and completely eliminates β–ketoacyl synthase activity. Seffernick et al. (J. Bacteriol. 183(8):2405-2410, 2001) teaches that two naturally occurring Pseudomonas

enzymes having 98% amino acid sequence identity catalyze two different reactions: deamination and dehalogenation, therefore having different function. Therefore, the claimed genera of polypeptides have the potentiality of encompassing many different functions.

In addition, while a sufficient written description of a genus of polypeptides may be achieved by a recitation of a representative number of polypeptides defined by their sequence or a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus, in the instant case, the interpreted structural feature, "any fragment of SEQ ID NO: 6", does not constitute a substantial portion of the genus as the remainder of any polypeptide comprising said structural elements is completely undefined and the specification does not define the remaining structural features for members of the genus to be selected. Many functionally and structurally unrelated polypeptides are encompassed by these claims. The specification only discloses a single species of the claimed genus which is insufficient to put one of ordinary skill in the art in possession of all attributes and features of all species within the claimed genus. Therefore, one skilled in the art cannot reasonably conclude that the applicant had possession of the claimed invention at the time the instant application was filed.

16. Even if specific and substantial utility or well established utility is found for the polypeptide of SEQ ID NO: 6, the following rejection applies. Claims 1, 29 and 32 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for the polypeptide of SEQ ID NO: 6, and the polypeptide of SEQ ID NO: 6 lacking its N-terminal Met residue or its signal peptide, does not reasonably provide enablement for (1) a polypeptide of any function comprising any fragment of the polypeptide of SEQ ID NO: 6, (2) a pharmaceutical composition comprising the polypeptide of SEQ ID NO: 6, or (3) a pharmaceutical composition comprising a polypeptide of any function comprising any fragment of the polypeptide of SEQ ID NO: 6. The specification does not enable any person skilled in

the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

The criteria for undue experimentation, summarized in *re Wands*, 8, USPQ2nd 1400 (Fed. Cir. 1988) are: 1) quantity of experimentation necessary, 2) the amount of direction or guidance presented, 3) the presence and absence of working examples, 4) the nature of the invention, 5) the state of prior art, 6) the relative skill of those in the art, 7) the predictability or unpredictability of the art, and 8) the breath of the claims.

The scope of the claims is not commensurate with the enablement provided in regard to the extremely large number of polypeptides of unknown function and structure encompassed by the claims, as well as unknown diseases which can be treated with said polypeptides. As indicated above, while the specification discloses the structure of the polypeptide of SEQ ID NO:6 and indicates that this polypeptide is an aortic carboxypeptidase-like protein (ACPL) 2, the specification is completely silent in regard to (1) the structures and functions of all the polypeptides comprising any fragment of the polypeptide of SEQ ID NO: 6, (2) which fragments of the polypeptide of SEQ ID NO: 6 are required in any polypeptide such that it can display the same function as that of the polypeptide of SEQ ID NO: 6, and (3) diseases that can be effectively treated using a "pharmaceutical composition" comprising the claimed polypeptides.

While one could argue that the genus of polypeptides comprising any fragment of the polypeptide of SEQ ID NO: 6 is enabled since one could make those polypeptides, as indicated above, the state of the art teaches the unpredictability of assigning function based solely on structural homology and discloses examples of how even small structural changes can lead to major changes in function. See the teachings of Seffernick et al., and Witkowski et al. already discussed. Therefore, while one of skill in the art can make these polypeptides, determining the function of such polypeptides without undue experimentation would require some knowledge or guidance as to how structure correlates with the desired function.

In regard to pharmaceutical compositions comprising the recited polypeptides, it is noted that the term "pharmaceutical" implies a treatment of a disease, and based on the information provided in the specification, it is unpredictable as to which diseases can be effectively treated using a "pharmaceutical composition" comprising the claimed polypeptides. Neither the specification nor the prior art provide sufficient guidance as to what specific diseases could be successfully treated by administering a "pharmaceutical composition" comprising the recited polypeptides, and attempting to identify a disease treatable using such a "pharmaceutical composition" would constitute undue experimentation. The specification merely provides a statement indicating that the proteins disclosed in the specification have potential therapeutic applications for treating hypertensive disorders and/or vascular endothelial disorders. (page 19, last paragraph). There is no indication or evidence that administering therapeutic dosages of the polypeptide of SEQ ID NO: 6 would have any use in treating these disorders beyond mere speculation. Furthermore, even if the specification had provided sufficient guidance as to a disease treatable by administering a "pharmaceutical composition" comprising the polypeptide of SEQ ID NO:6, the specification provides no guidance as to what, besides such polypeptide, would compose such a composition. Making and testing the infinite number of compositions to find one that is effective would constitute undue experimentation.

Therefore, due to the lack of relevant examples, the amount of information provided, the lack of knowledge about the critical structural elements required to display the desired function, the unpredictability of the prior art in regard to function based on homology, and the lack of knowledge as to the specific diseases which can be treated by pharmaceutical compositions comprising the recited polypeptides, the specific dosages and additional compounds in such composition, one of ordinary skill in the art would have to go through the burden of undue experimentation in order to (1) determine the actual function of any polypeptide comprising any fragment of the polypeptide of SEQ ID NO: 6, (2) determine the specific diseases which can be treated with the polypeptides recited in the claims, and (3) determine

dosage and additional ingredients required in the pharmaceutical compositions claimed. Thus, Applicant has not provided sufficient guidance to enable one of ordinary skill in the art to make and use the invention in a manner reasonably correlated with the scope of the claims.

Claim Rejections - 35 USC § 102

17. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless -

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

18. Claim 1 is rejected under 35 U.S.C. 102(a) as being anticipated by Ota et al. (EMBL accession number BAB55275; TrEMBL accession number Q96SM3; Q9NUB5; May 2001; cited in the IDS). Claim 1 (as interpreted) is directed to a polypeptide comprising any fragment of the polypeptide of SEQ ID NO: 6. Ota et al. teaches a protein comprising amino acids 1-509 and 510-574 of the polypeptide of SEQ ID NO: 6, therefore anticipating the instant claim as interpreted. See attached alignment provided for visualization purposes.

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

19. Claim 1 is rejected under 35 U.S.C. 102(b) as being anticipated by Layne et al. (J.Biol. Chem. 273(25):15654-15660, 1998; cited in the IDS). Claim 1 (as interpreted) is directed to a polypeptide comprising any fragment of the polypeptide of SEQ ID NO: 6. Layne et al. teaches a human aortic carboxypeptidase-like protein comprising several fragments of the polypeptide of SEQ ID NO: 6, therefore anticipating the instant claim as interpreted. See attached alignment provided for visualization purposes.

Conclusion

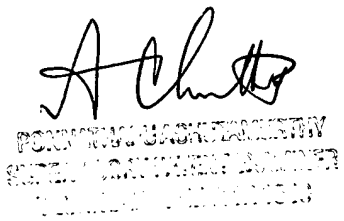
20. No claim is in condition for allowance.

21. Certain papers related to this application may be submitted to Art Unit 1652 by facsimile transmission. The FAX number is (703) 872-9306. The faxing of such papers must conform with the notices published in the Official Gazette, 1156 OG 61 (November 16, 1993) and 1157 OG 94 (December 28, 1993) (see 37 CFR 1.6(d)). NOTE: If Applicant submits a paper by FAX, the original copy should be retained by Applicant or Applicant's representative. NO DUPLICATE COPIES SHOULD BE SUBMITTED, so as to avoid the processing of duplicate papers in the Office.

22. Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PMR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

23. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Delia M. Ramirez whose telephone number is (571) 272-0938. The examiner can normally be reached on Monday-Friday from 8:30 AM to 5:00 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Dr. Ponnathapura Achutamurthy can be reached on (571) 272-0928. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (571) 272-1600.



Delia M. Ramirez, Ph.D.
Patent Examiner
Art Unit 1652

DR
January 21, 2005

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RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC063430; AAH63430.1; -.
KW   Carboxypeptidase.
SQ   SEQUENCE   734 AA;  81693 MW;  D5FFC614FE356102 CRC64;

  Query Match             96.9%;  Score 2974;  DB 2;  Length 734;
  Best Local Similarity   78.1%;  Pred. No. 7.2e-209;
  Matches  573;  Conservative    0;  Mismatches    1;  Indels  160;  Gaps    1;

Qy          1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
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Qy         61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120
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Qy        121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
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Qy        181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240
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Db        181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240

Qy        241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300
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Qy        421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR 480
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Qy        481 AVIKWMKRIPFVLSANLHGGELVVSYPFD---------------------------- 509
              ||||||||||||||||||||||||||||
Db        481 AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540

Qy        510 ------------------------------------------------------------ 509

Db        541 LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600

Qy        510 ------------------------------------------------------------ 509

Db        601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY 660

Qy        510 ---------MVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP 560
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Db        661 WRLLTPGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP 720

Qy        561 DLRRRLERLRGQKD 574
              ||||||||||||||
Db        721 DLRRRLERLRGQKD 734


RESULT 5
CPXM_HUMAN
ID   CPXM_HUMAN     STANDARD;      PRT;   734 AA.
AC   Q96SM3; Q9NUB5;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Potential carboxypeptidase X precursor (EC 3.4.17.-)
DE   (Metallocarboxypeptidase CPX-1).
GN   Name=CPXM;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Teratocarcinoma;
RX   PubMed=14702039; DOI=10.1038/ng1285;
RA   Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA   Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA   Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA   Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA   Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA   Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA   Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA   Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA   Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA   Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA   Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA   Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA   Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA   Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA   Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA   Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA   Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA   Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA   Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA   Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA   Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA   Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA   Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA   Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA   Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA   Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA   Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA   Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA   Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA   Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA   Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
RN   [3]
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RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Embryonic brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX   PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA   Hillman R.T., Green R.E., Brenner S.E.;
RT   "An unappreciated role for RNA surveillance.";
RL   Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
CC   -!- FUNCTION: May be involved in cell-cell interactions. No
CC       carboxypeptidase activity was found yet (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q96SM3-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q96SM3-2; Sequence=VSP_000780, VSP_000781;
CC         Note=May be produced at very low levels due to a premature stop
CC         codon in the mRNA, leading to nonsense-mediated mRNA decay. No
CC         experimental confirmation available;
CC   -!- SIMILARITY: Belongs to peptidase family M14.
CC   -!- SIMILARITY: Contains 1 F5/8 type C domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AK027661; BAB55275.1; -.
DR   EMBL; AL035460; CAB82246.1; -.
DR   EMBL; BC032692; AAH32692.1; -.
DR   HSSP; Q90240; 1H8L.
DR   MEROPS; M14.015; -.
DR   Genew; HGNC:15771; CPXM.
DR   InterPro; IPR008969; CarboxypepD_reg.
DR   InterPro; IPR000421; FA58_C.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR000834; Peptidase_M14.
DR   InterPro; IPR008575; Peptidase_M14B.
DR   Pfam; PF05885; DUF857; 1.
DR   Pfam; PF00754; F5_F8_type_C; 1.
DR   Pfam; PF00246; Zn_carbOpept; 1.
DR   PRINTS; PR00765; CRBOXYPTASEA.
DR   SMART; SM00231; FA58C; 1.
DR   SMART; SM00631; Zn_pept; 1.
DR   PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.
DR   PROSITE; PS00133; CARBOXYPEPT_ZN_2; 1.
DR   PROSITE; PS01285; FA58C_1; FALSE_NEG.
DR   PROSITE; PS01286; FA58C_2; FALSE_NEG.
DR   PROSITE; PS50022; FA58C_3; 1.
KW   Alternative splicing; Carboxypeptidase; Glycoprotein; Hydrolase;
KW   Metalloprotease; Signal; Zinc.
FT   SIGNAL        1    20       Potential.
FT   CHAIN        21   734       Potential carboxypeptidase X.
FT   DOMAIN      113   274       F5/8 type C.
FT   DOMAIN       70    73       Poly-Lys.
FT   DOMAIN      369   373       Poly-Leu.
FT   METAL       360   360       Zinc (By similarity).
FT   METAL       363   363       Zinc (By similarity).
FT   METAL       498   498       Zinc (By similarity).
FT   ACT_SITE    591   591       Nucleophile (By similarity).
FT   DISULFID    115   274       By similarity.
FT   CARBOHYD     57    57       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    210   210       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    220   220       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    318   318       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    428   428       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    472   472       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    308   356       LMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHEL
FT                               GEPEVRYV -> VRYNPYDLGRRAHPSQVPFPPSHRGTTCC
FT                               DCACMPLLPPDVSAFSPVDP (in isoform 2).
FT                               /FTId=VSP_000780.
FT   VARSPLIC    357   734       Missing (in isoform 2).
FT                               /FTId=VSP_000781.
FT   CONFLICT    390   390       W -> R (in Ref. 2).
SQ   SEQUENCE   734 AA;  81697 MW;  815705578E8A58F3 CRC64;
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  Query Match             96.8%;  Score 2972;  DB 1;  Length 734;
  Best Local Similarity   78.1%;  Pred. No. 1e-208;
  Matches  573;  Conservative    0;  Mismatches    1;  Indels  160;  Gaps    1;

Qy          1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Qy         61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120

Qy        121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180

Qy        181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240

Qy        241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300

Qy        301 NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360

Qy        361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GNEALGRELLLLLMQFLCHEFLRGNPRVTWLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420

Qy        421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR 480

Qy        481 AVIKWMKRIPFVLSANLHGGELVVSYPFD---------------------------- 509
              ||||||||||||||||||||||||||||
Db        481 AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540

Qy        510 ------------------------------------------------------------ 509

Db        541 LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600

Qy        510 ------------------------------------------------------------ 509
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601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY 660

510 ---------MVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
661 WRLLTPGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP 720

561 DLRRRLERLRGQKD 574
    ||||||||||||||
721 DLRRRLERLRGQKD 734
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SULT 6
N2E1
    Q8N2E1      PRELIMINARY;      PRT;   477 AA.
    Q8N2E1;
    01-OCT-2002 (TrEMBLrel. 22, Created)
    01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
    Hypothetical protein PSEC0226.
    Homo sapiens (Human).
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    NCBI_TaxID=9606;
    [1]
    SEQUENCE FROM N.A.
    TISSUE=Whole embryo;
    Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
    Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
    Nagahari K., Sugano S., Isogai T.;
    Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
R   EMBL; AK075527; BAC11672.1; -.
R   HSSP; Q90240; 1H8L.
R   GO; GO:0004182; F:carboxypeptidase A activity; IEA.
R   GO; GO:0004180; F:carboxypeptidase activity; IEA.
R   GO; GO:0007155; P:cell adhesion; IEA.
R   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R   InterPro; IPR000421; FA58_C.
R   InterPro; IPR008979; Gal_bind_like.
R   InterPro; IPR000834; Peptidase_M14.
R   Pfam; PF00754; F5_F8_type_C; 1.
R   Pfam; PF00246; Zn_carbOpept; 1.
R   PRINTS; PR00765; CRBOXYPTASEA.
R   SMART; SM00231; FA58C; 1.
R   SMART; SM00631; Zn_pept; 1.
R   PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.
R   PROSITE; PS50022; FA58C_3; 1.
KW  Carboxypeptidase.
SQ  SEQUENCE   477 AA;  52766 MW;  0A3FBE477B57A246 CRC64;

  Query Match          81.1%;  Score 2491;  DB 2;  Length 477;
  Best Local Similarity  99.8%;  Pred. No. 9e-174;
  Matches  464;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Qy         61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120

Qy        121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180

Qy        181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240

Qy        241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300
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Qy        301 NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360

Qy        361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420

Qy        421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLP 465
              |||||||||||||||||||||||||||||||||||||||||||| |
Db        421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPQP 465
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RESULT 7
CPXM_MOUSE
ID   CPXM_MOUSE      STANDARD;      PRT;   722 AA.
AC   Q9Z100; Q99LA3;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Potential carboxypeptidase X precursor (EC 3.4.17.-)
DE   (Metallocarboxypeptidase CPX-1).
GN   Name=Cpxm; Synonyms=Cpxm1, Cpx1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RC   TISSUE=Heart;
RX   MEDLINE=99171585; PubMed=10073577;
RA   Lei Y., Xin X., Morgan D., Pintar J.E., Fricker L.D.;
RT   "Identification of mouse CPX-1, a novel member of the
RT   metallocarboxypeptidase gene family with highest similarity to CPX-
RT   2.";
RL   DNA Cell Biol. 18:175-185(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: May be involved in cell-cell interactions. No
CC       carboxypeptidase activity was found yet.
CC   -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC   -!- TISSUE SPECIFICITY: Strongly expressed in testis and spleen.
CC       Moderatly expressed in salivary gland, brain, heart, lung, and
CC       kidney. Extremely low expression in liver and muscle. No
CC       expression in eye, adrenal, and white adipose tissues.
CC   -!- DEVELOPMENTAL STAGE: First expressed at 13.5 dpc, in the meninges,
CC       nasal mesenchyme, primordial cartilage and skeletal structures.
CC   -!- SIMILARITY: Belongs to peptidase family M14.
CC   -!- SIMILARITY: Contains 1 F5/8 type C domain.
CC   ---------------------------------------------------------------------
```

```
  Matches  246;  Conservative   75;  Mismatches  134;  Indels  195;  Gaps    6;

Qy        107 PAEKQETGCPPLGLESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAE 166
              | || :  |||:|:|| |: |::: |||    |||  |||||:|:|  : | ||||||||
Db        370 PVEKIK--CPPIGMESHRIEDNQIRASSMLRHGLGAQRGRLNMQAGANEDDYYDGAWCAE 427

Qy        167 EQDADPWFQVDAGHPTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMD 226
              ::    | :||    |||:|||||||:|    |:||:: | |||||:||    |    |
Db        428 DESQTQWIEVDTRRTTRFTGVITQGRDSSIHDDFVTTFFVGFSNDSQTWVMYTNGYEEM- 486

Qy        227 AVFPANSDPETPVLNLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEA 286
              |  | | :|||: |||| |||||: | ||   |: |:| |:| |||:        : :
Db        487 -TFYGNVDKDTPVLSELPEPVVARFIRIYPLTW--NGSLCMRLEVLGCPVTPVYSYYAQN 543

Qy        287 PASGSSDPLDFQHHNYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEH 346
              ::| |||:||:|| ||:||| | |:|| ||| ||:||| :|||:| ||:|| ||:|
Db        544 EVV-TTDSLDFRHHSYKDMRQLMKAVNEECPTITRTYSLGKSSRGLKIYAMEISDNPGDH 602

Qy        347 ELGEPEVRYVAGMHGNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPD 406
              |||||| || ||:|||| ||||||||||||:|| |:  |||||  |: : ||||:||:|||
Db        603 ELGEPEFRYTAGIHGNEVLGRELLLLLMQYLCQEYRDGNPRVRNLVQDTRIHLVPSLNPD 662

Qy        407 GYEIAYHRGSELVGWAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPT 466
              |||:|   |||   || | |  :  |: :| |||: || |::   ||: |||::||:|
Db        663 GYEVAAQMGSEFGNWALGLWTEEGFDIFEDFPDLNSVLWAAEEKKWVPYRVPNNNLPIPE 722

Qy        467 YYTLPNATVAPETRAVIKWMKRIPFVLSANLHGGELVVSYPFDM---------------- 510
              |  |:|||: | ||:| ||:: |||| |||:||| :||||:||
Db        723 RYLSPDATVSTEVRAIISWMEKNPFVLGANLNGGERLVSYPYDMARTPSQEQLLAEALAA 782

Qy        511 ------------------------------------------------------------ 510

Db        783 ARGEDDDGVSEAQETPDHAIFRWLAISFASAHLTMTEPYRGGCQAQDYTSGMGIVNGAKW 842

Qy        511 ------------------------------------------------------------ 510

Db        843 NPRSGTFNDFSYLHTNCLELSVYLGCDKFPHESELPREWENNKEALLTFMEQVHRGIKGV 902

Qy        511 ----------------------------------------VTASAEGYHSVTRNCRVTF 529
                                                       ||| |||| |  : | | :
Db        903 VTDEQGIPIANATISVSGINHGVKTASGGDYWRILNPGEYRVTAHAEGYTSSAKICNVDY 962

Qy        530 EEGPFPCNFVLTKTPKQRLRELLAAGAKVP-----------PDLRRRLER 568
              : |   |||:| ::  :|:||:||     |           |  ||  :|
Db        963 DIGATQCNFILARSNWKRIREILAMNGNRPILGVDPSRPMTPQQRRMQQR 1012


RESULT 12
Q7KZ79
ID   Q7KZ79      PRELIMINARY;      PRT;   845 AA.
AC   Q7KZ79;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   AEBP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cancellous bone;
RX   MEDLINE=97079196; PubMed=8920928;
RA   Ohno I., Hashimoto J., Shimizu K., Takaoka K., Ochi T., Matsubara K.,
RA   Okubo K.;
RT   "A cDNA cloning of human AEBP1 from primary cultured osteoblasts and
RT   its expression in a differentiating osteoblastic cell line.";
RL   Biochem. Biophys. Res. Commun. 228:411-414(1996).
DR   EMBL; D86479; BAA13094.1; -.
DR   InterPro; IPR008969; CarboxypepD_reg.
DR   InterPro; IPR000421; FA58_C.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR000834; Peptidase_M14.
DR   InterPro; IPR008575; Peptidase_M14B.
DR   Pfam; PF05885; DUF857; 1.
DR   Pfam; PF00754; F5_F8_type_C; 1.
DR   Pfam; PF00246; Zn_carbOpept; 1.
DR   PRINTS; PR00765; CRBOXYPTASEA.
DR   SMART; SM00231; FA58C; 1.
DR   SMART; SM00631; Zn_pept; 1.
DR   PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.
DR   PROSITE; PS01285; FA58C_1; 1.
DR   PROSITE; PS01286; FA58C_2; UNKNOWN_1.
DR   PROSITE; PS50022; FA58C_3; 1.
SQ   SEQUENCE   845 AA;  96173 MW;  3378DA64C413F120 CRC64;

  Query Match             38.0%;  Score 1166;  DB 2;  Length 845;
  Best Local Similarity   37.7%;  Pred. No. 1.9e-76;
  Matches  249;  Conservative   74;  Mismatches  136;  Indels  202;  Gaps    8;

Qy        107 PAEKQETGCPPLGLESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAE 166
              | || :  |||:|:|| |: |::: |||    |||  |||||:|:|  : | ||||||||
Db         66 PTEKVK--CPPIGMESHRIEDNQIRASSMLRHGLGAQRGRLNMQTGATEDDYYDGAWCAE 123

Qy        167 EQDADPWFQVDAGHPTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMD 226
              :    | :||    |||:|||||||:|    |:||:: | |||||:||    |    |
Db        124 DDARTQWIEVDTRRTTRFTGVITQGRDSSIHDDFVTTFFVGFSNDSQTWVMYTNGYEEM- 182

Qy        227 AVFPANSDPETPVLNLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEA 286
              |  | | :|||: |||| |||||: | ||   |: |:| |:| | |:        : :
Db        183 -TFHGNVDKDTPVLSELPEPVVARFIRIYPLTW--NGSLCMRLEVLGCSVAPVYSYYAQN 239

Qy        287 PASGSSDPLDFQHHNYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEH 346
              ::| |||:||:|| ||:||| | |:|| ||| ||:||| :|||:| ||:|| ||||
Db        240 EVV-ATDDLDFRHHSYKDMRQLMKVVNEECPTITRTYSLGKSSRGLKIYAMEISDNPGEH 298

Qy        347 ELGEPEVRYVAGMHGNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPD 406
              |||||| || ||:|||| ||||||||||||:|| |:  |||||  |: : ||||:||:|||
Db        299 ELGEPEFRYTAGIHGNEVLGRELLLLLMQYLCREYRDGNPRVRSLVQDTRIHLVPSLNPD 358

Qy        407 GYEIAYHRGSELVGWAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPT 466
              |||:|   |||   || | |  :  |:  :| |||: || |::   ||: |||::||:|
Db        359 GYEVAAQMGSEFGNWALGLWTEEGFDIFEDFPDLNSVLWGAEERKWVPYRVPNNNLPIPE 418

Qy        467 YYTLPNATVAPETRAVIKWMKRIPFVLSANLHGGELVVSYPFDM---------------- 510
              |  |:|||: | ||:| ||:: |||| |||:||| :||||:||
Db        419 RYLSPDATVSTEVRAIIAWMEKNPFVLGANLNGGERLVSYPYDMARTPTQEQLLAAAMAA 478

Qy        511 ------------------------------------------------------------ 510

Db        479 ARGEDEDEVSEAQETPDHAIFRWLAISFASAHLTLTEPYRGGCQAQDYTGGMGIVNGAKW 538

Qy        511 ------------------------------------------------------------ 510

Db        539 NPRTGTINDFSYLHTNCLELSFYLGCDKFPHESELPREWENNKEALLTFMEQVHRGIKGV 598

Qy        511 ----------------------------------------VTASAEGYHSVTRNCRVTF 529
                                                       ||| |||    : | | :
Db        599 VTDEQGIPIANATISVSGINHGVKTASGGDYWRILNPGEYRVTAHAEGYTPSAKTCNVDY 658

Qy        530 EEGPFPCNFVLTKTPKQRLRELLAAGAKVP-----------PDLR----RRLE---RLRG 571
              : |   |||:| ::  :|:||::|     |           |  |    |||:   |||
Db        659 DIGATQCNFILARSNWKRIREIMAMNGNRPIPHIDPSRPMTPQQRRLQQRRLQHRLRLRA 718

Qy        572 Q 572
              |
Db        719 Q 719


RESULT 13
Q14113
ID   Q14113      PRELIMINARY;      PRT;  1158 AA.
AC   Q14113;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
```

```
Aortic carboxypeptidase-like protein ACLP.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Aorta smooth muscle;
MEDLINE=98288305; PubMed=9624159;
Layne M.D., Endege W.O., Jain M.K., Yet S.F., Hsieh C.M., Chin M.T.,
Perrella M.A., Blanar M.A., Haber E., Lee M.E.;
"Aortic carboxypeptidase-like protein, a novel protein with discoidin
and carboxypeptidase-like domains, is up-regulated during vascular
smooth muscle cell differentiation.";
J. Biol. Chem. 273:15654-15660(1998).
EMBL; AF053944; AAC25585.1; -.
PIR; JC5256; JC5256.
HSSP; Q90240; 1H8L.
MEROPS; M14.951; -.
Genew; HGNC:303; AEBP1.
GO; GO:0004180; F:carboxypeptidase activity; TAS.
GO; GO:0003700; F:transcription factor activity; TAS.
GO; GO:0007517; P:muscle development; TAS.
GO; GO:0001501; P:skeletal development; TAS.
InterPro; IPR000421; FA58_C.
InterPro; IPR008979; Gal_bind_like.
InterPro; IPR000834; Peptidase_M14.
InterPro; IPR008575; Peptidase_M14B.
Pfam; PF05885; DUF857; 1.
Pfam; PF00754; F5_F8_type_C; 1.
Pfam; PF00246; Zn_carbOpept; 1.
PRINTS; PR00765; CRBOXYPTASEA.
SMART; SM00231; FA58C; 1.
SMART; SM00631; Zn_pept; 1.
PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.
PROSITE; PS01285; FA58C_1; 1.
PROSITE; PS01286; FA58C_2; UNKNOWN_1.
PROSITE; PS50022; FA58C_3; 1.
Carboxypeptidase.
SEQUENCE   1158 AA;  130901 MW;  3BFC06B6A4971F30 CRC64;

  Query Match           38.0%;  Score 1166;  DB 2;  Length 1158;
  Best Local Similarity  37.7%;  Pred. No. 3e-76;
  Matches  249;  Conservative   74;  Mismatches  136;  Indels  202;  Gaps    8;

Qy        107 PAEKQETGCPPLGLESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAE 166
              | ||  :  |||:|:|| |: |::: |||    |||  |||||:|:|   : | ||||||||
Db        379 PTEKVK--CPPIGMESHRIEDNQIRASSMLRHGLGAQRGRLNMQTGATEDDYYDGAWCAE 436

Qy        167 EQDADPWFQVDAGHPTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMD 226
              :    | :||    |||:|||||||:|    |:||:: | |||||:||     |    |
Db        437 DDARTQWIEVDTRRTTRFTGVITQGRDSSIHDDFVTTFFVGFSNDSQTWVMYTNGYEEM- 495

Qy        227 AVFPANSDPETPVLNLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEA 286
                | | :||||: |||| ||||||: | ||    |: |:| |:| | |:       : :
Db        496 -TFHGNVDKDTPVLSELPEPVVARFIRIYPLTW--NGSLCMRLEVLGCSVAPVYSYYAQN 552

Qy        287 PASGSSDPLDFQHHNYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEH 346
                ::| |||:||:|| ||:||| | |:|| ||| ||:||| :|||:| ||:|| ||||
Db        553 EVV-ATDDLDFRHHSYKDMRQLMKVVNEECPTITRTYSLGKSSRGLKIYAMEISDNPGEH 611

Qy        347 ELGEPEVRYVAGMHGNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPD 406
              |||||| || ||:|||| |||||||||||:|| |:  |||||  |: : ||||:|||:|||
Db        612 ELGEPEFRYTAGIHGNEVLGRELLLLLMQYLCREYRDGNPRVRSLVQDTRIHLVPSLNPD 671

Qy        407 GYEIAYHRGSELVGWAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPT 466
              |||:|   |||   || | |  :  |:  :| |||: || |::   ||: |||::||:|
Db        672 GYEVAAQMGSEFGNWALGLWTEEGFDIFEDFPDLNSVLWGAEERKWVPYRVPNNNLPIPE 731

Qy        467 YYTLPNATVAPETRAVIKWMKRIPFVLSANLHGGELVVSYPFDM---------------- 510
              |  |:|||: | ||:| ||:: |||| |||:|||| :||||:||
Db        732 RYLSPDATVSTEVRAIIAWMEKNPFVLGANLNGGERLVSYPYDMARTPTQEQLLAAAMAA 791

Qy        511 ------------------------------------------------------------ 510

Db        792 ARGEDEDEVSEAQETPDHAIFRWLAISFASAHLTLTEPYRGGCQAQDYTGGMGIVNGAKW 851

Qy        511 ------------------------------------------------------------ 510

Db        852 NPRTGTINDFSYLHTNCLELSFYLGCDKFPHESELPREWENNKEALLTFMEQVHRGIKGV 911

Qy        511 ----------------------------------------VTASAEGYHSVTRNCRVTF 529
                                                       ||| ||||    : | | :
Db        912 VTDEQGIPIANATISVSGINHGVKTASGGDYWRILNPGEYRVTAHAEGYTPSAKTCNVDY 971

Qy        530 EEGPFPCNFVLTKTPKQRLRELLAAGAKVP----------PDLR----RRLE---RLRG 571
              : |   |||:| ::  :|:||::|     |          | |     |||:   |||
Db        972 DIGATQCNFILARSNWKRIREIMAMNGNRPIPHIDPSRPMTPQQRRLQQRRLQHRLRLRA 1031

Qy        572 Q 572
              |
Db       1032 Q 1032


RESULT 14
Q8IUX7
ID   Q8IUX7      PRELIMINARY;      PRT;  1158 AA.
AC   Q8IUX7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Adipocyte enhancer binding protein 1,.
GN   Name=AEBP1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC038588; AAH38588.1; -.
DR   HSSP; Q90240; 1H8L.
DR   MEROPS; M14.951; -.
DR   GO; GO:0004182; F:carboxypeptidase A activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR000421; FA58_C.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR000834; Peptidase_M14.
```